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TECH CENTER 1600/2900



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1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/695,423

DATE: 01/30/2003

TIME: 13:24:06

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3 <110> APPLICANT: KATO, MASARU
 4 MIURA, YUTAKA
 5 KETTOKU, MASAKO
 6 IWAMATSU, AKIHIRO
 7 KOBAYASHI, KAZUO
 8 KOMEDA, TOSHIHIRO
 10 <120> TITLE OF INVENTION: NOVEL TRANSFERASE AND AMYLASE, PROCESS FOR PRODUCING
 11 THE ENZYMES, USE THEREOF, AND GENE CODING FOR THE SAME
 13 <130> FILE REFERENCE: 049441/0124
 15 <140> CURRENT APPLICATION NUMBER: 09/695,423
 C--> 16 <141> CURRENT FILING DATE: 2003-01-24
 18 <150> PRIOR APPLICATION NUMBER: 09/298,924
 19 <151> PRIOR FILING DATE: 1999-04-26
 21 <150> PRIOR APPLICATION NUMBER: 08/750,569
 22 <151> PRIOR FILING DATE: 1997-02-24
 24 <150> PRIOR APPLICATION NUMBER: PCT/JP95/01189
 25 <151> PRIOR FILING DATE: 1995-06-14
 27 <150> PRIOR APPLICATION NUMBER: JP 7-120673
 28 <151> PRIOR FILING DATE: 1995-04-21
 30 <150> PRIOR APPLICATION NUMBER: JP 6-311185
 31 <151> PRIOR FILING DATE: 1994-11-21
 33 <150> PRIOR APPLICATION NUMBER: JP 6-286917
 34 <151> PRIOR FILING DATE: 1994-11-21
 36 <150> PRIOR APPLICATION NUMBER: JP 6-290394
 37 <151> PRIOR FILING DATE: 1994-10-31
 39 <150> PRIOR APPLICATION NUMBER: JP 6-194223
 40 <151> PRIOR FILING DATE: 1994-08-18
 42 <150> PRIOR APPLICATION NUMBER: JP 6-133354
 43 <151> PRIOR FILING DATE: 1994-06-16
 45 <160> NUMBER OF SEQ ID NOS: 63
 47 <170> SOFTWARE: PatentIn Ver. 2.1
 49 <210> SEQ ID NO: 1
 50 <211> LENGTH: 2578
 51 <212> TYPE: DNA
 52 <213> ORGANISM: Sulfolobus solfataricus
 54 <220> FEATURE:
 55 <221> NAME/KEY: CDS
 56 <222> LOCATION: (335)..(2518)
 58 <400> SEQUENCE: 1
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 63 ttaacatcta tggagagaga attgcggatg attcattctt gataattctt aacgcaaadc 180
 65 ccaataacgt aaaagtgaag ttcccaaagg gtaaatggga actagttgtt ggttcttatt 240

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67 tgagagagat aaaaccagaa gaaagaattg tagaaggatga gaaggaattg gaaattgagg 300
69 gaagaacagc attagtttat aggaggacag aact atg ata ata ggc aca tat agg 355
70                                     Met Ile Ile Gly Thr Tyr Arg
71                                     1           5
73 ctg caa ctc aat aag aaa ttc act ttt tac gat ata ata gaa aat ttg 403
74 Leu Gln Leu Asn Lys Lys Phe Thr Phe Tyr Asp Ile Ile Glu Asn Leu
75                                     10          15          20
77 gat tat ttt aaa gaa tta gga gta tca cac cta tat cta tct cca ata 451
78 Asp Tyr Phe Lys Glu Leu Gly Val Ser His Leu Tyr Leu Ser Pro Ile
79                                     25          30          35
81 ctt aag gct aga cca ggg agc act cac ggc tac gat gta gta gat cat 499
82 Leu Lys Ala Arg Pro Gly Ser Thr His Gly Tyr Asp Val Val Asp His
83 40          45          50          55
85 agt gaa att aat gag gaa tta gga gga gaa gag ggg tgc ttt aaa cta 547
86 Ser Glu Ile Asn Glu Glu Leu Gly Gly Glu Glu Gly Cys Phe Lys Leu
87                                     60          65          70
89 gtt aag gaa gct aag agt aga ggt tta gaa atc ata caa gat ata gtg 595
90 Val Lys Glu Ala Lys Ser Arg Gly Leu Glu Ile Ile Gln Asp Ile Val
91                                     75          80          85
93 cca aat cac atg gcg gta cat cat act aat tgg aga ctt atg gat ctg 643
94 Pro Asn His Met Ala Val His His Thr Asn Trp Arg Leu Met Asp Leu
95                                     90          95          100
97 tta aag agt tgg aag aat agt aaa tac tat aac tat ttt gat cac tac 691
98 Leu Lys Ser Trp Lys Asn Ser Lys Tyr Tyr Asn Tyr Phe Asp His Tyr
99                                     105         110         115
101 gat gat gac aag ata atc ctc cca ata ctt gag gac gag ttg gat acc 739
102 Asp Asp Asp Lys Ile Ile Leu Pro Ile Leu Glu Asp Glu Leu Asp Thr
103 120          125          130          135
105 gtt ata gat aag gga ttg ata aaa cta cag aag gat aat ata gag tac 787
106 Val Ile Asp Lys Gly Leu Ile Lys Leu Gln Lys Asp Asn Ile Glu Tyr
107                                     140          145          150
109 aga ggg ctt ata tta cct ata aat gat gaa gga gtt gaa ttc ttg aaa 835
110 Arg Gly Leu Ile Leu Pro Ile Asn Asp Glu Gly Val Glu Phe Leu Lys
111                                     155          160          165
113 agg att aat tgc ttt gat aat tca tgt tta aag aaa gag gat ata aag 883
114 Arg Ile Asn Cys Phe Asp Asn Ser Cys Leu Lys Lys Glu Asp Ile Lys
115                                     170          175          180
117 aaa tta cta tta ata caa tat tat cag cta act tac tgg aag aaa ggt 931
118 Lys Leu Leu Leu Ile Gln Tyr Tyr Gln Leu Thr Tyr Trp Lys Lys Gly
119                                     185          190          195
121 tat cca aac tat agg aga ttt ttc gca gta aat gat ttg ata gct gtt 979
122 Tyr Pro Asn Tyr Arg Arg Phe Phe Ala Val Asn Asp Leu Ile Ala Val
123 200          205          210          215
125 agg gta gaa ttg gat gaa gta ttt aga gag tcc cat gag ata att gct 1027
126 Arg Val Glu Leu Asp Glu Val Phe Arg Glu Ser His Glu Ile Ile Ala
127                                     220          225          230
129 aag cta cca gtt gac ggt tta aga att gac cac ata gat gga cta tat 1075
130 Lys Leu Pro Val Asp Gly Leu Arg Ile Asp His Ile Asp Gly Leu Tyr
131                                     235          240          245

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133 aac cct aag gag tat tta gat aag cta aga cag tta gta gga aat gat 1123
134 Asn Pro Lys Glu Tyr Leu Asp Lys Leu Arg Gln Leu Val Gly Asn Asp
135      250      255      260
137 aag ata ata tac gta gag aag ata ttg tca atc aac gag aaa tta aga 1171
138 Lys Ile Ile Tyr Val Glu Lys Ile Leu Ser Ile Asn Glu Lys Leu Arg
139      265      270      275
141 gat gat tgg aaa gta gat ggg act act gga tat gat ttc ttg aac tac 1219
142 Asp Asp Trp Lys Val Asp Gly Thr Thr Gly Tyr Asp Phe Leu Asn Tyr
143 280      285      290      295
145 gtt aat atg cta tta gta gat gga agt ggt gag gag gta act aag 1267
146 Val Asn Met Leu Leu Val Asp Gly Ser Gly Glu Glu Leu Thr Lys
147      300      305      310
149 ttt tat gag aat ttc att gga agg aaa atc aat ata gac gag tta ata 1315
150 Phe Tyr Glu Asn Phe Ile Gly Arg Lys Ile Asn Ile Asp Glu Leu Ile
151      315      320      325
153 ata caa agt aaa aaa tta gtt gca aat cag tta ttt aaa ggt gac att 1363
154 Ile Gln Ser Lys Lys Leu Val Ala Asn Gln Leu Phe Lys Gly Asp Ile
155      330      335      340
157 gaa aga tta agc aag tta ctg aac gtt aat tac gat tat tta gta gat 1411
158 Glu Arg Leu Ser Lys Leu Leu Asn Val Asn Tyr Asp Tyr Leu Val Asp
159      345      350      355
161 ttt cta gca tgt atg aaa aaa tac agg act tat tta cca tat gag gat 1459
162 Phe Leu Ala Cys Met Lys Lys Tyr Arg Thr Tyr Leu Pro Tyr Glu Asp
163 360      365      370      375
165 att aac gga ata agg gaa tgc gat aag gag gga aag tta aaa gat gaa 1507
166 Ile Asn Gly Ile Arg Glu Cys Asp Lys Glu Gly Lys Leu Lys Asp Glu
167      380      385      390
169 aag gga atc atg aga ctc caa caa tac atg cca gca atc ttc gct aag 1555
170 Lys Gly Ile Met Arg Leu Gln Gln Tyr Met Pro Ala Ile Phe Ala Lys
171      395      400      405
173 ggc tat gag gat act acc ctc ttc atc tac aat aga tta att tcc ctt 1603
174 Gly Tyr Glu Asp Thr Thr Leu Phe Ile Tyr Asn Arg Leu Ile Ser Leu
175      410      415      420
177 aac gag gtt ggg agc gac cta aga aga ttc agt tta agc atc aaa gac 1651
178 Asn Glu Val Gly Ser Asp Leu Arg Arg Phe Ser Leu Ser Ile Lys Asp
179      425      430      435
181 ttt cat aac ttt aac cta agc aga gta aat acc ata tca atg aac act 1699
182 Phe His Asn Phe Asn Leu Ser Arg Val Asn Thr Ile Ser Met Asn Thr
183 440      445      450      455
185 ctt tcc act cat gat act aaa ttc agt gaa gac gtt aga gct aga ata 1747
186 Leu Ser Thr His Asp Thr Lys Phe Ser Glu Asp Val Arg Ala Arg Ile
187      460      465      470
189 tca gta cta tct gag ata cca aag gag tgg gag gag agg gta ata tac 1795
190 Ser Val Leu Ser Glu Ile Pro Lys Glu Trp Glu Glu Arg Val Ile Tyr
191      475      480      485
193 tgg cat gat ttg tta agg cca aat att gat aaa aac gat gag tat aga 1843
194 Trp His Asp Leu Leu Arg Pro Asn Ile Asp Lys Asn Asp Glu Tyr Arg
195      490      495      500
197 ttt tat caa aca ctt gtg gga agt tac gag gga ttt gat aat aag gag 1891

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198 Phe Tyr Gln Thr Leu Val Gly Ser Tyr Glu Gly Phe Asp Asn Lys Glu
199      505                      510                      515
201 aga att aag aac cac atg att aag gtc ata aga gaa gct aag gta cat 1939
202 Arg Ile Lys Asn His Met Ile Lys Val Ile Arg Glu Ala Lys Val His
203 520                      525                      530                      535
205 aca acg tgg gaa aat cct aat ata gag tat gaa aag aag gtt ctg ggt 1987
206 Thr Thr Trp Glu Asn Pro Asn Ile Glu Tyr Glu Lys Lys Val Leu Gly
207      540                      545                      550
209 ttc ata gat gaa gtg ttc gag aac agt aat ttt aga aat gat ttt gaa 2035
210 Phe Ile Asp Glu Val Phe Glu Asn Ser Asn Phe Arg Asn Asp Phe Glu
211      555                      560                      565
213 aat ttt gaa aag aaa ata gtt tat ttc ggt tat atg aaa tca tta atc 2083
214 Asn Phe Glu Lys Lys Ile Val Tyr Phe Gly Tyr Met Lys Ser Leu Ile
215      570                      575                      580
217 gca acg aca ctt agg ttc ctt tcg ccc ggt gta cca gat att tat caa 2131
218 Ala Thr Thr Leu Arg Phe Leu Ser Pro Gly Val Pro Asp Ile Tyr Gln
219      585                      590                      595
221 gga act gaa gtt tgg aga ttc tta ctt aca gac cca gat aac aga atg 2179
222 Gly Thr Glu Val Trp Arg Phe Leu Leu Thr Asp Pro Asp Asn Arg Met
223 600                      605                      610                      615
225 ccg gtg gat ttc aag aaa cta aag gaa tta tta aat aat ttg act gaa 2227
226 Pro Val Asp Phe Lys Lys Leu Lys Glu Leu Leu Asn Asn Leu Thr Glu
227      620                      625                      630
229 aag aac tta gaa ctc tca gat cca aga gtc aaa atg tta tat gtt aag 2275
230 Lys Asn Leu Glu Leu Ser Asp Pro Arg Val Lys Met Leu Tyr Val Lys
231      635                      640                      645
233 aaa ttg cta cag ctt aga aga gag tac tca cta aac gat tat aaa cca 2323
234 Lys Leu Leu Gln Leu Arg Arg Glu Tyr Ser Leu Asn Asp Tyr Lys Pro
235      650                      655                      660
237 ttg ccc ttt ggc ttc caa agg gga aaa gta gct gtc ctt ttc tca cca 2371
238 Leu Pro Phe Gly Phe Gln Arg Gly Lys Val Ala Val Leu Phe Ser Pro
239      665                      670                      675
241 ata gtg act agg gag gtt aaa gag aaa att agt ata agg caa aaa agc 2419
242 Ile Val Thr Arg Glu Val Lys Glu Lys Ile Ser Ile Arg Gln Lys Ser
243 680                      685                      690                      695
245 gtt gat tgg atc aga aat gag gaa att agt agt gga gaa tac aat tta 2467
246 Val Asp Trp Ile Arg Asn Glu Glu Ile Ser Ser Gly Glu Tyr Asn Leu
247      700                      705                      710
249 agt gag ttg att ggg aag cat aaa gtc gtt ata tta act gaa aaa agg 2515
250 Ser Glu Leu Ile Gly Lys His Lys Val Val Ile Leu Thr Glu Lys Arg
251      715                      720                      725
253 gag tgaactacct acatagattt attcttgaac tactctggtc agaaatgtat 2568
254 Glu
256 tacgcagatc 2578
259 <210> SEQ ID NO: 2
260 <211> LENGTH: 728
261 <212> TYPE: PRT
262 <213> ORGANISM: Sulfolobus solfataricus
264 <400> SEQUENCE: 2

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265 Met Ile Ile Gly Thr Tyr Arg Leu Gln Leu Asn Lys Lys Phe Thr Phe
266   1           5           10           15
268 Tyr Asp Ile Ile Glu Asn Leu Asp Tyr Phe Lys Glu Leu Gly Val Ser
269           20           25           30
271 His Leu Tyr Leu Ser Pro Ile Leu Lys Ala Arg Pro Gly Ser Thr His
272           35           40           45
274 Gly Tyr Asp Val Val Asp His Ser Glu Ile Asn Glu Glu Leu Gly Gly
275           50           55           60
277 Glu Glu Gly Cys Phe Lys Leu Val Lys Glu Ala Lys Ser Arg Gly Leu
278           65           70           75           80
280 Glu Ile Ile Gln Asp Ile Val Pro Asn His Met Ala Val His His Thr
281           85           90           95
283 Asn Trp Arg Leu Met Asp Leu Leu Lys Ser Trp Lys Asn Ser Lys Tyr
284           100          105          110
286 Tyr Asn Tyr Phe Asp His Tyr Asp Asp Asp Lys Ile Ile Leu Pro Ile
287           115          120          125
289 Leu Glu Asp Glu Leu Asp Thr Val Ile Asp Lys Gly Leu Ile Lys Leu
290           130          135          140
292 Gln Lys Asp Asn Ile Glu Tyr Arg Gly Leu Ile Leu Pro Ile Asn Asp
293          145          150          155          160
295 Glu Gly Val Glu Phe Leu Lys Arg Ile Asn Cys Phe Asp Asn Ser Cys
296           165          170          175
298 Leu Lys Lys Glu Asp Ile Lys Lys Leu Leu Leu Ile Gln Tyr Tyr Gln
299           180          185          190
301 Leu Thr Tyr Trp Lys Lys Gly Tyr Pro Asn Tyr Arg Arg Phe Phe Ala
302           195          200          205
304 Val Asn Asp Leu Ile Ala Val Arg Val Glu Leu Asp Glu Val Phe Arg
305           210          215          220
307 Glu Ser His Glu Ile Ile Ala Lys Leu Pro Val Asp Gly Leu Arg Ile
308          225          230          235          240
310 Asp His Ile Asp Gly Leu Tyr Asn Pro Lys Glu Tyr Leu Asp Lys Leu
311           245          250          255
313 Arg Gln Leu Val Gly Asn Asp Lys Ile Ile Tyr Val Glu Lys Ile Leu
314           260          265          270
316 Ser Ile Asn Glu Lys Leu Arg Asp Asp Trp Lys Val Asp Gly Thr Thr
317           275          280          285
319 Gly Tyr Asp Phe Leu Asn Tyr Val Asn Met Leu Leu Val Asp Gly Ser
320           290          295          300
322 Gly Glu Glu Glu Leu Thr Lys Phe Tyr Glu Asn Phe Ile Gly Arg Lys
323          305          310          315          320
325 Ile Asn Ile Asp Glu Leu Ile Ile Gln Ser Lys Lys Leu Val Ala Asn
326           325          330          335
328 Gln Leu Phe Lys Gly Asp Ile Glu Arg Leu Ser Lys Leu Leu Asn Val
329           340          345          350
331 Asn Tyr Asp Tyr Leu Val Asp Phe Leu Ala Cys Met Lys Lys Tyr Arg
332           355          360          365
334 Thr Tyr Leu Pro Tyr Glu Asp Ile Asn Gly Ile Arg Glu Cys Asp Lys
335           370          375          380
337 Glu Gly Lys Leu Lys Asp Glu Lys Gly Ile Met Arg Leu Gln Gln Tyr

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VERIFICATION SUMMARY

PATENT APPLICATION: **US/09/695,423**

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date